

FIGURE 1B: V_H DOMAIN

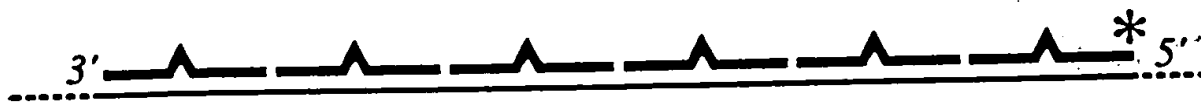
	10	20	30	40	50	A
4D5	EVQLQQSGPELVKPGASLKL	SCTASGFNIKDTYIHWVKQRPEQGLEWIGRIYPTN				
HU4D5	EVQLVESGGGLVQPGGSLRLS	CAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTN				
HUV _H III	EVQLVESGGGLVQPGGSLRLS	CAASGFTFSDYAMSWVRQAPGKGLEWVAVISENG				
		-----				-----
			V _H -CDR1			V _H -CDR2

	60	70	80	ABC	90	100ABC
4D5	GYTRYDPKFQDKATITADTSSNTAYLQVSRLTSEDTAVYYCSRWGGDGFYAMDYW					
HU4D5	GYTRYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDVW					
HUV _H III	SDTYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCARDRGGAVSFYFDVW					
	-----					-----
						V _H -CDR3

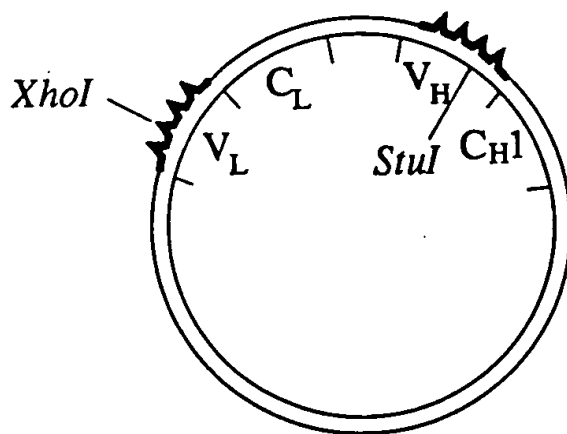
	110
4D5	GQGASVTVSS
HU4D5	GQGTLVTVSS
HUV _H III	GQGTLVTVSS

FIGURE 2

Anneal huV_L or huV_H oligomers to pAK1 template



1. Ligate
2. Isolate assembled oligomers
3. Anneal to pAK1 template (*XhoI*⁻, *StuI*⁺)
4. Extend and ligate



1. Transform *E. coli*
2. Isolate phagemid pool
3. Enrich for huV_L and huV_H (*XhoI*⁺, *StuI*⁻)
4. Sequence verify

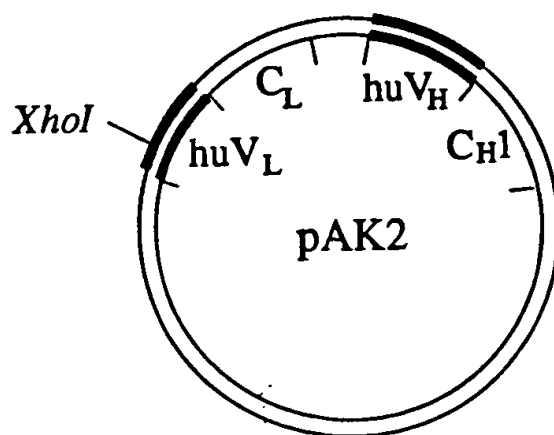


FIGURE 3

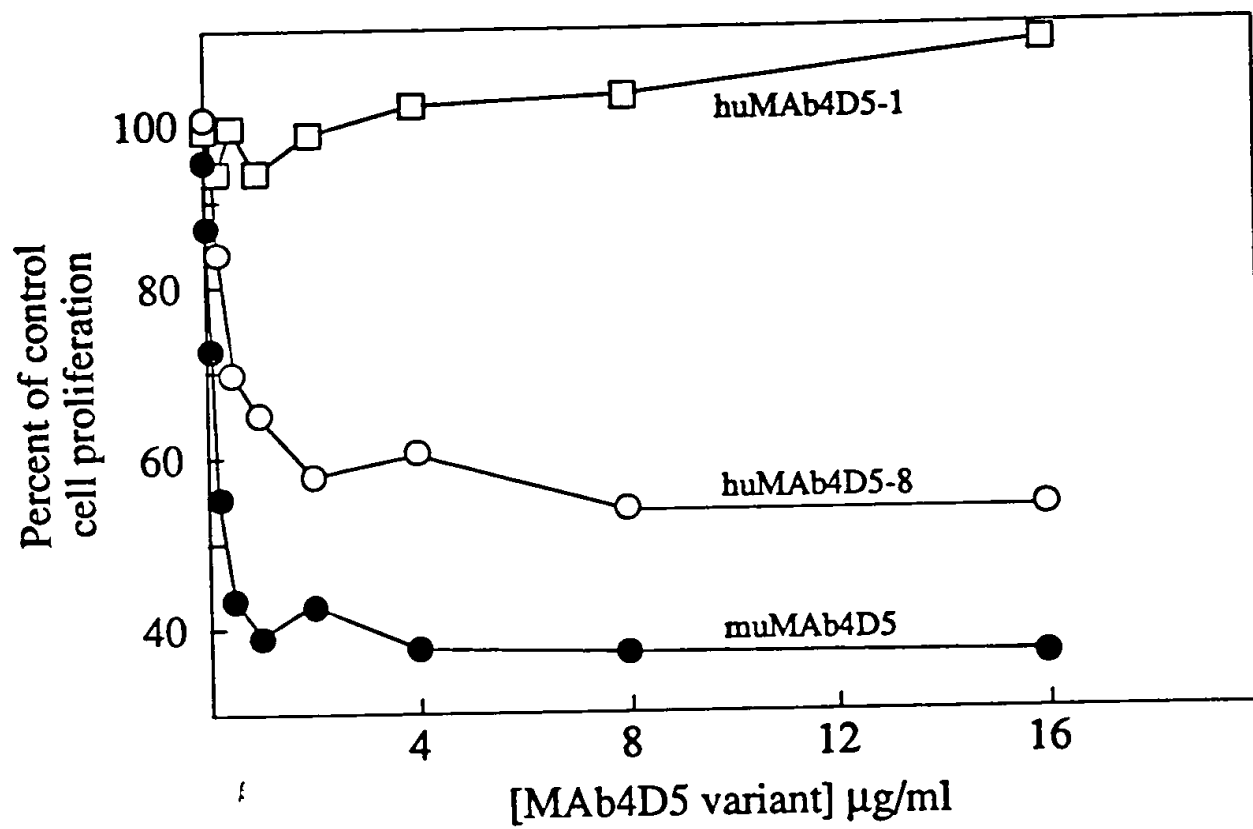


FIGURE 4

